

SEQUENCE LISTING

<110> Fletcher, Jonathan A.  
Kroll, Todd G.

<120> PAX8-PPARGgamma NUCLEIC ACID MOLECULES  
AND POLYPEPTIDES AND USES THEREOF

<130> B0801/7196 (ERP/MAT)

<150> US 60/177,109

<151> 2000-01-20

<150> US 60/225,079

<151> 2000-08-14

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<170> FastSEQ for Windows Version 3.0

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<211> 2334

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

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gga ggg gcc ttt gtg aat ggc aga cct ctg ccg gaa gtg gtc cgc cag	96
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln	
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cgc atc gta gac ctg gcc cac cag ggt gta agg ccc tgc gac atc tct	144
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser	
35 40 45	
cgc cag ctc cgc gtc agc cat ggc tgc gtc agc aag atc ctt ggc agg	192
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg	
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tac tac gag act ggc agc atc cgg cct gga gtg ata ggg ggc tcc aag	240
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys	
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ccc aag gtg gcc acc ccc aag gtg gtg gag aag att ggg gac tac aaa	288
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys	
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09765441.011001

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Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu	
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 gct gag ggc gtc tgt gac aat gac act gtg ccc agt gtc agc tcc att	384
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile	
115 120 125	
 aat aga atc atc cgg acc aaa gtg cag caa cca ttc aac ctc cct atg	432
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met	
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 gac agc tgc gtg gcc acc aag tcc ctg agt ccc gga cac acg ctg atc	480
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile	
145 150 155 160	
 ccc agc tca gct gta act ccc ccg gag tca ccc cag tcg gat tcc ctg	528
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu	
165 170 175	
 ggc tcc acc tac tcc atc aat ggg ctc ctg ggc atc gct cag cct ggc	576
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly	
180 185 190	
 agc gac aag agg aaa atg gat gac agt gat cag gat agc tgc cga cta	624
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu	
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 agc att gac tca cag agc agc agc agc gga ccc cga aag cac ctt cgc	672
Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg	
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Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe	
225 230 235 240	
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Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys	
245 250 255	
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Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp	
260 265 270	
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Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn	
275 280 285	
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Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Glu Met Thr Met Val	
290 295 300	
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Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val	
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ttc act act gtt gac ttc tcc agc att tct act cca cat tac gaa gac	1056
Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp	
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Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp	
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ctg aaa ctt caa gag tac caa agt gca atc aaa gtg gag cct gca tct	1152
Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser	
370 375 380	
cca cct tat tat tct gag aag act cag ctc tac aat aag cct cat gaa	1200
Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu	
385 390 395 400	
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Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp	
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Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys	
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Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys	
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gat ctt aac tgt cgg atc cac aaa aaa agt aga aat aaa tgt cag tac	1392
Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr	
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Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile	
465 470 475 480	
agg ttt ggg cgg atg cca cag gcc gag aag gag aag ctg ttg gcg gag	1488
Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu	
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Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg	
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gcc ctg gca aaa cat ttg tat gac tca tac ata aag tcc ttc ccg ctg	1584
Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu	
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Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys	
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Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu	
565 570 575	
gtg gcc atc cgc atc ttt cag ggc tgc cag ttt cgc tcc gtg gag gct	1776
Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala	
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Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn	
595 600 605	
ctt gac ttg aac gac caa gta act ctc ctc aaa tat gga gtc cac gag	1872
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cga aag cct ttt ggt gac ttt atg gag ccc aag ttt gag ttt gct gtg	2016
Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val	
660 665 670	
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Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile	
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Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu	
725 730 735	
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Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu	
740 745 750	
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2334

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Pro	Lys	Val	Ala	Thr	Pro	Lys	Val	Val	Glu	Lys	Ile	Gly	Asp	Tyr	Lys
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Ser	Ile	Asp	Ser	Gln	Ser	Ser	Ser	Ser	Gly	Pro	Arg	Lys	His	Leu	Arg
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Asp	Leu	Ser	Val	Met	Glu	Asp	His	Ser	His	Ser	Phe	Asp	Ile	Lys	Pro
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Pro Pro Tyr Tyr Ser Glu	Lys Thr Gln Leu Tyr	Asn Lys Pro His Glu
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Lys Ala Ser Gly Phe His	Tyr Gly Val His Ala	Cys Glu Gly Cys Lys
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Cys Arg Phe Gln Lys Cys	Leu Ala Val Gly Met	Ser His Asn Ala Ile
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Lys Ile Lys Phe Lys His	Ile Thr Pro Leu Gln	Glu Gln Ser Lys Glu
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Arg Lys Pro Phe Gly Asp	Phe Met Glu Pro Lys	Phe Glu Phe Ala Val
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Lys Phe Asn Ala Leu Glu	Leu Asp Asp Ser Asp	Leu Ala Ile Phe Ile
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Ala Val Ile Ile Leu Ser	Gly Asp Arg Pro Gly	Leu Leu Asn Val Lys
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Pro Ile Glu Asp Ile Gln	Asp Asn Leu Leu Gln	Ala Leu Glu Leu Gln
705	710	715
Leu Lys Leu Asn His Pro	Glu Ser Ser Gln Leu	Phe Ala Lys Leu Leu
725	730	735
Gln Lys Met Thr Asp Leu	Arg Gln Ile Val Thr	Glu His Val Gln Leu
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gga ggg gcc ttt gtg aat ggc aga cct ctg ccg gaa gtg gtc cgc cag	96
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln	
20 25 30	
cgc atc gta gac ctg gcc cac cag ggt gta agg ccc tgc gac atc tct	144
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser	
35 40 45	
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Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg	
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tac tac gag act ggc agc atc cgg cct gga gtg ata ggg ggc tcc aag	240
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys	
65 70 75 80	
ccc aag gtg gcc acc ccc aag gtg gtg gag aag att ggg gac tac aaa	288
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys	
85 90 95	
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Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu	
100 105 110	
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Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile	
115 120 125	
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Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met	
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Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile	
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Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu	
165 170 175	
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Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly	
180 185 190	

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Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser Pro	
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Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly	
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ttc ttc cgg aga aca atc aga ttg aag ctt atc tat gac aga tgt gat	1536
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Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu Val	
625 630 635 640	

006511 01504

gcc atc cgc atc ttt cag ggc tgc cag ttt cgc tcc gtg gag gct gtg	1968
Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala Val	
645 650 655	
cag gag atc aca gag tat gcc aaa agc att cct ggt ttt gta aat ctt	2016
Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn Leu	
660 665 670	
gac ttg aac gac caa gta act ctc ctc aaa tat gga gtc cac gag atc	2064
Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ile	
675 680 685	
att tac aca atg ctg gcc tcc ttg atg aat aaa gat ggg gtt ctc ata	2112
Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile	
690 695 700	
tcc gag ggc caa ggc ttc atg aca agg gag ttt cta aag agc ctg cga	2160
Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg	
705 710 715 720	
aag cct ttt ggt gac ttt atg gag ccc aag ttt gag ttt gct gtg aag	2208
Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys	
725 730 735	
ttc aat gca ctg gaa tta gat gac agc gac ttg gca ata ttt att gct	2256
Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala	
740 745 750	
gtc att att ctc agt gga gac cgc cca ggt ttg ctg aat gtg aag ccc	2304
Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys Pro	
755 760 765	
att gaa gac att caa gac aac ctg cta caa gcc ctg gag ctc cag ctg	2352
Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln Leu	
770 775 780	
aag ctg aac cac cct gag tcc tca cag ctg ttt gcc aag ctg ctc cag	2400
Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu Gln	
785 790 795 800	
aaa atg aca gac ctc aga cag att gtc acg gaa cac gtg cag cta ctg	2448
Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu Leu	
805 810 815	
cag gtg atc aag aag acg gag aca gac atg agt ctt cac ccg ctc ctg	2496
Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu Leu	
820 825 830	
cag gag atc tac aag gac ttg tac tag	2523
Gln Glu Ile Tyr Lys Asp Leu Tyr *	
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<213> Homo Sapiens

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Arg	Ile	Val	Asp	Leu	Ala	His	Gln	Gly	Val	Arg	Pro	Cys	Asp	Ile	Ser
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Arg	Gln	Leu	Arg	Val	Ser	His	Gly	Cys	Val	Ser	Lys	Ile	Leu	Gly	Arg
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Tyr	Tyr	Glu	Thr	Gly	Ser	Ile	Arg	Pro	Gly	Val	Ile	Gly	Gly	Ser	Lys
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Pro	Lys	Val	Ala	Thr	Pro	Lys	Val	Val	Glu	Lys	Ile	Gly	Asp	Tyr	Lys
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Arg	Gln	Asn	Pro	Thr	Met	Phe	Ala	Trp	Glu	Ile	Arg	Asp	Arg	Leu	Leu
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Ala	Glu	Gly	Val	Cys	Asp	Asn	Asp	Thr	Val	Pro	Ser	Val	Ser	Ser	Ile
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Asn	Arg	Ile	Ile	Arg	Thr	Lys	Val	Gln	Gln	Pro	Phe	Asn	Leu	Pro	Met
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Asp	Ser	Cys	Val	Ala	Thr	Lys	Ser	Leu	Ser	Pro	Gly	His	Thr	Leu	Ile
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Pro	Ser	Ser	Ala	Val	Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	Asp	Ser	Leu
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Gly	Ser	Thr	Tyr	Ser	Ile	Asn	Gly	Leu	Leu	Gly	Ile	Ala	Gln	Pro	Gly
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Ser	Asp	Lys	Arg	Lys	Met	Asp	Asp	Ser	Asp	Gln	Asp	Ser	Cys	Arg	Leu
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Ser	Ile	Asp	Ser	Gln	Ser	Ser	Ser	Ser	Gly	Pro	Arg	Lys	His	Leu	Arg
	210					215					220				
Thr	Asp	Ala	Phe	Ser	Gln	His	His	Leu	Glu	Pro	Leu	Glu	Cys	Pro	Phe
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Glu	Arg	Gln	His	Tyr	Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys
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Gly	Glu	Gln	Gly	Leu	Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp
		260					265						270		
Asp	Gly	Lys	Ala	Thr	Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	Gly	Arg	Asn
		275				280						285			
Leu	Ser	Thr	His	Gln	Thr	Tyr	Pro	Val	Val	Ala	Asp	Pro	His	Ser	Pro
	290					295					300				
Leu	Ala	Ile	Lys	Gln	Glu	Thr	Pro	Glu	Val	Ser	Ser	Ser	Ser	Ser	Thr
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Pro	Cys	Ser	Leu	Ser	Ser	Ser	Ala	Leu	Leu	Asp	Leu	Gln	Gln	Val	Gly
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Ser	Gly	Val	Pro	Phe	Asn	Ala	Phe	Pro	His	Ala	Ala	Ser	Val	Tyr	
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Gly	Gln	Phe	Thr	Gly	Gln	Ala	Leu	Ser	Glu	Met	Thr	Met	Val	Asp	
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Thr	Glu	Met	Pro	Phe	Trp	Pro	Thr	Asn	Phe	Gly	Ile	Ser	Ser	Val	Asp
	370					375					380				
Leu	Ser	Val	Met	Glu	Asp	His	Ser	His	Ser	Phe	Asp	Ile	Lys	Pro	Phe
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Thr	Thr	Val	Asp	Phe	Ser	Ser	Ile	Ser	Thr	Pro	His	Tyr	Glu	Asp	Ile
			405					410					415		
Pro	Phe	Thr	Arg	Thr	Asp	Pro	Val	Val	Ala	Asp	Tyr	Lys	Tyr	Asp	Leu

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Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu Glu		
450	455	460
Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp Lys		
465	470	475
Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly		
485	490	495
Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys Asp		
500	505	510
Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr Cys		
515	520	525
Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile Arg		
530	535	540
Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu Ile		
545	550	555
Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg Ala		
565	570	575
Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu Thr		
580	585	590
Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys Ser		
595	600	605
Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp Lys		
610	615	620
Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu Val		
625	630	635
Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala Val		
645	650	655
Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn Leu		
660	665	670
Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ile		
675	680	685
Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile		
690	695	700
Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg		
705	710	715
Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys		
725	730	735
Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala		
740	745	750
Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys Pro		
755	760	765
Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln Leu		
770	775	780
Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu Gln		
785	790	795
Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu Leu		
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Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu Leu		
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Gln Glu Ile Tyr Lys Asp Leu Tyr		
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Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln	
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Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser	
35 40 45	
cgc cag ctc cgc gtc agc cat ggc tgc gtc agc aag atc ctt ggc agg	192
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg	
50 55 60	
tac tac gag act ggc agc atc cgg cct gga gtg ata ggg ggc tcc aag	240
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys	
65 70 75 80	
ccc aag gtg gcc acc ccc aag gtg gtg gag aag att ggg gac tac aaa	288
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys	
85 90 95	
cgc cag aac cct acc atg ttt gcc tgg gag atc cga gac cgg ctc ctg	336
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu	
100 105 110	
gct gag ggc gtc tgt gac aat gac act gtg ccc agt gtc agc tcc att	384
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile	
115 120 125	
aat aga atc atc cgg acc aaa gtg cag caa cca ttc aac ctc cct atg	432
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met	
130 135 140	
gac agc tgc gtg gcc acc aag tcc ctg agt ccc gga cac acg ctg atc	480
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile	
145 150 155 160	
ccc agc tca gct gta act ccc ccg gag tca ccc cag tcg gat tcc ctg	528
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu	
165 170 175	
ggc tcc acc tac tcc atc aat ggg ctc ctg ggc atc gct cag cct ggc	576
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly	
180 185 190	

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agc att gac tca cag agc agc agc agc gga ccc cga aag cac ctt cgc	672
Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg	
210 215 220	
acg gat gcc ttc agc cag cac cac ctc gag ccg ctc gag tgc cca ttt	720
Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe	
225 230 235 240	
gag cgg cag cac tac cca gag gcc tat gcc tcc ccc agc cac acc aaa	768
Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys	
245 250 255	
ggc gag cag ggc ctc tac ccg ctg ccc ttg ctc aac agc acc ctg gac	816
Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp	
260 265 270	
gac ggg aag gcc acc ctg acc cct tcc aac acg cca ctg ggg cgc aac	864
Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn	
275 280 285	
ctc tcg act cac cag acc tac ccc gtg gtg gca gat cct cac tca ccc	912
Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro His Ser Pro	
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Leu Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser Ser Ser Thr	
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Pro Cys Ser Leu Ser Ser Ser Ala Leu Leu Asp Leu Gln Gln Val Gly	
325 330 335	
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Ser Gly Val Pro Pro Phe Asn Ala Phe Pro His Ala Ala Ser Val Tyr	
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Gly Gln Phe Thr Gly Gln Ala Leu Leu Ser Gly Arg Glu Met Val Gly	
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Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly	
370 375 380	
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Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Glu Met Thr Met	
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Val Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser	
405 410 415	

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Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys	
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Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu	
435 440 445	
gac att cca ttc aca aga aca gat cca gtg gtt gca gat tac aag tat	1392
Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr	
450 455 460	
gac ctg aaa ctt caa gag tac caa agt gca atc aaa gtg gag cct gca	1440
Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala	
465 470 475 480	
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Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His	
485 490 495	
gaa gag cct tcc aac tcc ctc atg gca att gaa tgt cgt gtc tgt gga	1536
Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly	
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Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys	
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Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg	
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Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln	
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Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala	
565 570 575	
atc agg ttt ggg cgg atg cca cag gcc gag aag gag aag ctg ttg gcg	1776
Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala	
580 585 590	
gag atc tcc agt gat atc gac cag ctg aat cca gag tcc gct gac ctc	1824
Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu	
595 600 605	
cgg gcc ctg gca aaa cat ttg tat gac tca tac ata aag tcc ttc ccg	1872
Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro	
610 615 620	
ctg acc aaa gca aag gcg agg gcg atc ttg aca gga aag aca aca gac	1920
Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp	
625 630 635 640	

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Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys	
660 665 670	
gag gtg gcc atc cgc atc ttt cag ggc tgc cag ttt cgc tcc gtg gag	2064
Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu	
675 680 685	
gct gtg cag gag atc aca gag tat gcc aaa agc att cct ggt ttt gta	2112
Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val	
690 695 700	
aat ctt gac ttg aac gac caa gta act ctc ctc aaa tat gga gtc cac	2160
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gag atc att tac aca atg ctg gcc tcc ttg atg aat aaa gat ggg gtt	2208
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725 730 735	
ctc ata tcc gag ggc caa ggc ttc atg aca agg gag ttt cta aag agc	2256
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Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala	
755 760 765	
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Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe	
770 775 780	
att gct gtc att att ctc agt gga gac cgc cca ggt ttg ctg aat gtg	2400
Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val	
785 790 795 800	
aag ccc att gaa gac att caa gac aac ctg cta caa gcc ctg gag ctc	2448
Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu	
805 810 815	
cag ctg aag ctg aac cac cct gag tcc tca cag ctg ttt gcc aag ctg	2496
Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu	
820 825 830	
ctc cag aaa atg aca gac ctc aga cag att gtc acg gaa cac gtg cag	2544
Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln	
835 840 845	
cta ctg cag gtg atc aag aag acg gag aca gac atg agt ctt cac ccg	2592
Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro	
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2625

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Arg	Ile	Val	Asp	Leu	Ala	His	Gln	Gly	Val	Arg	Pro	Cys	Asp	Ile	Ser
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Arg	Gln	Leu	Arg	Val	Ser	His	Gly	Cys	Val	Ser	Lys	Ile	Leu	Gly	Arg
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Tyr	Tyr	Glu	Thr	Gly	Ser	Ile	Arg	Pro	Gly	Val	Ile	Gly	Gly	Ser	Lys
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Pro	Lys	Val	Ala	Thr	Pro	Lys	Val	Val	Glu	Lys	Ile	Gly	Asp	Tyr	Lys
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Arg	Gln	Asn	Pro	Thr	Met	Phe	Ala	Trp	Glu	Ile	Arg	Asp	Arg	Leu	Leu
			100					105					110		
Ala	Glu	Gly	Val	Cys	Asp	Asn	Asp	Thr	Val	Pro	Ser	Val	Ser	Ser	Ile
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Asn	Arg	Ile	Ile	Arg	Thr	Lys	Val	Gln	Gln	Pro	Phe	Asn	Leu	Pro	Met
	130					135					140				
Asp	Ser	Cys	Val	Ala	Thr	Lys	Ser	Leu	Ser	Pro	Gly	His	Thr	Leu	Ile
145					150					155					160
Pro	Ser	Ser	Ala	Val	Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	Asp	Ser	Leu
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Gly	Ser	Thr	Tyr	Ser	Ile	Asn	Gly	Leu	Gly	Ile	Ala	Gln	Pro	Gly	
		180						185				190			
Ser	Asp	Lys	Arg	Lys	Met	Asp	Asp	Ser	Asp	Gln	Asp	Ser	Cys	Arg	Leu
	195						200					205			
Ser	Ile	Asp	Ser	Gln	Ser	Ser	Ser	Ser	Gly	Pro	Arg	Lys	His	Leu	Arg
	210					215					220				
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225					230					235					240
Glu	Arg	Gln	His	Tyr	Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys
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Gly	Glu	Gln	Gly	Leu	Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp
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Pro	Cys	Ser	Leu	Ser	Ser	Ser	Ala	Leu	Leu	Asp	Leu	Gln	Gln	Val	Gly
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Ser	Gly	Val	Pro	Pro	Phe	Asn	Ala	Phe	Pro	His	Ala	Ala	Ser	Val	Tyr
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Gly	Gln	Phe	Thr	Gly	Gln	Ala	Leu	Leu	Ser	Gly	Arg	Glu	Met	Val	Gly

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Pro Thr Leu	Pro Gly Tyr	Pro Thr Ser Gly Gln Gly
370	375	380
Ser Tyr Ala	Ser Ser Ala	Val Ala Glu Met Thr Met
385	390	395
Val Asp Thr	Glu Met Pro Phe Trp	Pro Thr Asn Phe Gly Ile Ser Ser
	405	410
Val Asp Leu	Ser Val Met Glu Asp	His Ser His Ser Phe Asp Ile Lys
	420	425
Pro Phe Thr	Thr Val Asp Phe Ser	Ser Ile Ser Thr Pro His Tyr Glu
	435	440
Asp Ile Pro	Phe Thr Arg Thr Asp	Pro Val Val Ala Asp Tyr Lys Tyr
	450	455
Asp Leu Lys	Leu Gln Glu Tyr Gln	Ser Ala Ile Lys Val Glu Pro Ala
	465	470
Ser Pro Pro	Tyr Tyr Ser Glu Lys	Thr Gln Leu Tyr Asn Lys Pro His
	485	490
Glu Glu Pro	Ser Asn Ser Leu Met	Ala Ile Glu Cys Arg Val Cys Gly
	500	505
Asp Lys Ala	Ser Gly Phe His Tyr	Gly Val His Ala Cys Glu Gly Cys
	515	520
Lys Gly Phe	Phe Arg Arg Thr Ile	Arg Leu Lys Leu Ile Tyr Asp Arg
	530	535
Cys Asp Leu	Asn Cys Arg Ile His	Lys Lys Ser Arg Asn Lys Cys Gln
	545	550
Tyr Cys Arg	Phe Gln Lys Cys Leu	Ala Val Gly Met Ser His Asn Ala
	565	570
Ile Arg Phe	Gly Arg Met Pro Gln	Ala Glu Lys Glu Lys Leu Leu Ala
	580	585
Glu Ile Ser	Ser Asp Ile Asp Gln	Leu Asn Pro Glu Ser Ala Asp Leu
	595	600
Arg Ala Leu	Ala Lys His Leu Tyr	Asp Ser Tyr Ile Lys Ser Phe Pro
	610	615
Leu Thr Lys	Ala Lys Ala Arg Ala	Ile Leu Thr Gly Lys Thr Thr Asp
	625	630
Lys Ser Pro	Phe Val Ile Tyr Asp	Met Asn Ser Leu Met Met Gly Glu
	645	650
Asp Lys Ile	Lys Phe Lys His Ile	Thr Pro Leu Gln Glu Gln Ser Lys
	660	665
Glu Val Ala	Ile Arg Ile Phe Gln	Gly Cys Gln Phe Arg Ser Val Glu
	675	680
Ala Val Gln	Glu Ile Thr Glu Tyr	Ala Lys Ser Ile Pro Gly Phe Val
	690	695
Asn Leu Asp	Leu Asn Asp Gln Val	Thr Leu Leu Lys Tyr Gly Val His
	705	710
Glu Ile Ile	Tyr Thr Met Leu Ala	Ser Leu Met Asn Lys Asp Gly Val
	725	730
Leu Ile Ser	Glu Gly Gln Gly Phe	Met Thr Arg Glu Phe Leu Lys Ser
	740	745
Leu Arg Lys	Pro Phe Gly Asp Phe	Met Glu Pro Lys Phe Glu Phe Ala
	755	760
Val Lys Phe	Asn Ala Leu Glu	Leu Asp Asp Ser Asp Leu Ala Ile Phe
	770	775
Ile Ala Val	Ile Ile Leu Ser	Gly Asp Arg Pro Gly Leu Leu Asn Val
	785	790
Lys Pro Ile	Glu Asp Ile Gln	Asp Asn Leu Leu Gln Ala Leu Glu Leu

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805 810 815  
 Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu  
 820 825 830  
 Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln  
 835 840 845  
 Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro  
 850 855 860  
 Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr  
 865 870

<210> 7  
 <211> 42  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> CDS  
 <222> (3)...(41)

<400> 7  
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 Thr Tyr Pro Val Val Ala Glu Met Thr Met Val Asp Thr  
 1 5 10

<210> 8  
 <211> 13  
 <212> PRT  
 <213> Homo Sapiens

<400> 8  
 Thr Tyr Pro Val Val Ala Glu Met Thr Met Val Asp Thr  
 1 5 10

<210> 9  
 <211> 42  
 <212> DNA  
 <213> Homo Sapiens

<220>  
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<400> 9  
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 Gly Gln Ala Leu Leu Ser Glu Met Thr Met Val Asp Thr  
 1 5 10

<210> 10  
 <211> 13  
 <212> PRT  
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<400> 10  
 Gly Gln Ala Leu Leu Ser Glu Met Thr Met Val Asp Thr

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5

10

<210> 11  
<211> 42  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> CDS  
<222> (3)...(41)

<400> 11

cc atc gca ggc atg gtg gca gaa atg acc atg gtt gac aca g 42  
Ile Ala Gly Met Val Ala Glu Met Thr Met Val Asp Thr  
1 5 10

<210> 12  
<211> 13  
<212> PRT  
<213> Homo Sapiens

<400> 12

Ile Ala Gly Met Val Ala Glu Met Thr Met Val Asp Thr  
1 5 10

<210> 13  
<211> 2711  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> CDS  
<222> (11)...(1363)

<400> 13

gaattcggcg atg cct cac aac tcc atc aga tct ggc cat gga ggg ctg 49  
Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu  
1 5 10

aac cag ctg gga ggg gcc ttt gtg aat ggc aga cct ctg ccg gaa gtg 97  
Asn Gln Leu Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val  
15 20 25

gtc cgc cag cgc atc gta gac ctg gcc cac cag ggt gta agg ccc tgc 145  
Val Arg Gln Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys  
30 35 40 45

gac atc tct cgc cag ctg cgc gtc agc cat ggt tgc gtc agc aag atc 193  
Asp Ile Ser Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile  
50 55 60

ctt ggc agg tac tac gag act ggc agc atc cgg cct gga gtg ata ggg 241  
Leu Gly Arg Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly  
65 70 75

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ggc tcc aag ccc aag gtg gcc acc ccc aag gtg gtg gag aag att ggg	289
Gly Ser Lys Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly	
80 85 90	
gac tac aaa cgc cag aac cct acc atg ttt gcc tgg gag atc cga gac	337
Asp Tyr Lys Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp	
95 100 105	
cgg ctg ctg gct gag ggc gtc tgt gac aat gac act gtg ccc agt gtc	385
Arg Leu Leu Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val	
110 115 120 125	
agc tcc att aat aga atc atc cgg acc aaa gtg cag caa cca ttc aac	433
Ser Ser Ile Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn	
130 135 140	
ctc cct atg gac agc tgc gtg gcc acc aag tcc ctg agt ccc gga cac	481
Leu Pro Met Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His	
145 150 155	
acg ctg atc ccc agc tca gct gta act ccc ccg gag tca ccc cag tcg	529
Thr Leu Ile Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser	
160 165 170	
gat tcc ctg ggc tcc acc tac tcc atc aat ggg ctg ctg ggc atc gct	577
Asp Ser Leu Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala	
175 180 185	
cag cct ggc agc gac aag agg aaa atg gat gac agt gat cag gat agc	625
Gln Pro Gly Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser	
190 195 200 205	
tgc cga cta agc att gac tca cag agc agc agc agc gga ccc cga aag	673
Cys Arg Leu Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys	
210 215 220	
cac ctt cgc acg gat gcc ttc agc cag cac cac ctg gag ccg ctg gag	721
His Leu Arg Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu	
225 230 235	
tgc cca ttt gag cgg cag cac tac cca gag gcc tat gcc tcc ccc agc	769
Cys Pro Phe Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser	
240 245 250	
cac acc aaa ggc gag cag ggc ctg tac ccg ctg ccc ttg ctg aac agc	817
His Thr Lys Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser	
255 260 265	
acc ctg gac gac ggg aag gcc acc ctg acc cct tcc aac acg cca ctg	865
Thr Leu Asp Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu	
270 275 280 285	
ggg cgc aac ctg tcg act cac cag acc tac ccc gtg gtg gca gat cct	913
Gly Arg Asn Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro	
290 295 300	

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cac tca ccc ttc gcc ata aag cag gaa acc ccc gag gtg tcc agt tct 961  
 His Ser Pro Phe Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser  
 305 310 315  
 agc tcc acc cct tcc tct tta tct agc tcc gcc ttt ttg gat ctg cag 1009  
 Ser Ser Thr Pro Ser Ser Leu Ser Ser Ser Ala Phe Leu Asp Leu Gln  
 320 325 330  
 caa gtc ggc tcc ggg gtc ccg ccc ttc aat gcc ttt ccc cat gct gcc 1057  
 Gln Val Gly Ser Gly Val Pro Pro Phe Asn Ala Phe Pro His Ala Ala  
 335 340 345  
 tcc gtg tac ggg cag ttc acg ggc cag gcc ctc ctc tca ggg cga gag 1105  
 Ser Val Tyr Gly Gln Phe Thr Gly Gln Ala Leu Leu Ser Gly Arg Glu  
 350 355 360 365  
 atg gtg ggg ccc acg ctg ccc gga tac cca ccc cac atc ccc acc agc 1153  
 Met Val Gly Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser  
 370 375 380  
 gga cag ggc agc tat gcc tcc tct gcc atc gca ggc atg gtg gca gga 1201  
 Gly Gln Gly Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Gly  
 385 390 395  
 agt gaa tac tct ggc aat gcc tat ggc cac acc ccc tac tcc tcc tac 1249  
 Ser Glu Tyr Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr  
 400 405 410  
 agc gag gcc tgg cgc ttc ccc aac tcc agc ttg ctg agt tcc cca tat 1297  
 Ser Glu Ala Trp Arg Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr  
 415 420 425  
 tat tac agt tcc aca tca agg ccg agt gca ccg ccc acc act gcc acg 1345  
 Tyr Tyr Ser Ser Thr Ser Arg Pro Ser Ala Pro Pro Thr Thr Ala Thr  
 430 435 440 445  
 gcc ttt gac cat ctg tag ttgaagctt 1372  
 Ala Phe Asp His Leu \*  
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<210> 14  
 <211> 450  
 <212> PRT  
 <213> Homo Sapiens

<400> 14  
 Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu  
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 Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln  
 20 25 30  
 Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser  
 35 40 45  
 Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg  
 50 55 60  
 Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys

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<221> CDS  
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<400> 15

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aattacagca	aaccctatt	ccatgctgtt	atg ggt gaa	act ctg gga	gat tct	114
			Met Gly	Glu Thr	Leu Gly Asp	
			1		5	
cct att gac	cca gaa agc	gat tcc ttc	act gat aca	ctg tct gca	aac	162
Ser						
ata tca caa	gaa atg acc	atg gtt gac	aca gag atg	cca ttc tgg	ccc	210
Pro Ile Asp	Pro Glu Ser	Asp Ser Phe	Thr Asp Thr	Leu Ser Ala	Asn	
10		15		20		
acc aac ttt	ggg atc agc	tcc gtg gat	ctc tcc gta	atg gaa gac	cac	258
Ile Ser Gln	Glu Met Thr	Met Val Asp	Thr Glu Met	Pro Phe Trp	Pro	
25		30		35	40	
tcc cac tcc	ttt gat atc	aag ccc ttc	act act gtt	gac ttc tcc	agc	306
Thr Asn Phe	Gly Ile Ser	Ser Val Asp	Leu Ser Val	Met Glu Asp	His	
	45		50		55	
att tct act	cca cat tac	gaa gac att	cca ttc aca	aga aca gat	cca	354
Ser His Ser	Phe Asp Ile	Lys Pro Phe	Thr Thr Val	Asp Phe Ser	Ser	
	60		65		70	
gtg gtt gca	gat tac aag	tat gac ctg	aaa ctt caa	gag tac caa	agt	402
Ile Ser Thr	Pro His Tyr	Glu Asp Ile	Pro Phe Thr	Arg Thr Asp	Pro	
	75		80		85	
gca atc aaa	gtg gag cct	gca tct cca	cct tat tat	tct gag aag	act	450
Val Val Ala	Asp Tyr Lys	Tyr Asp Leu	Lys Leu Gln	Glu Tyr Gln	Ser	
	90		95		100	
cag ctc tac	aat aag cct	cat gaa gag	cct tcc aac	tcc ctc atg	gca	498
Ala Ile Lys	Val Glu Pro	Ala Ser Pro	Pro Tyr Tyr	Ser Glu Lys	Thr	
105		110		115	120	
att gaa tgt	cgt gtc tgt	gga gat aaa	gct tct gga	ttt cac tat	gga	546
Gln Leu Tyr	Asn Lys Pro	His Glu Glu	Pro Ser Asn	Ser Leu Met	Ala	
	125		130		135	
gtt cat gct	tgt gaa gga	tgc aag ggt	ttc ttc cgg	aga aca atc	aga	594
Ile Glu Cys	Arg Val Cys	Gly Asp Lys	Ala Ser Gly	Phe His Tyr	Gly	
	140		145		150	
ttg aag ctt	atc tat gac	aga tgt gat	ctt aac tgt	cgg atc cac	aaa	642
Val His Ala	Cys Glu Gly	Cys Lys Gly	Phe Phe Arg	Arg Thr Ile	Arg	
	155		160		165	
aaa agt aga	aat aaa tgt	cag tac tgt	cgg ttt cag	aaa tgc ctt	gca	690
Leu Lys Leu	Ile Tyr Asp	Arg Cys Asp	Leu Asn Cys	Arg Ile His	Lys	
	170		175		180	

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gtg ggg atg tct cat aat gcc atc agg ttt ggg cgg atg cca cag gcc	738
Lys Ser Arg Asn Lys Cys Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala	
185 190 195 200	
gag aag gag aag ctg ttg gcg gag atc tcc agt gat atc gac cag ctg	786
Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met Pro Gln Ala	
205 210 215	
aat cca gag tcc gct gac ctc cgg gcc ctg gca aaa cat ttg tat gac	834
Glu Lys Glu Lys Leu Leu Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu	
220 225 230	
tca tac ata aag tcc ttc ccg ctg acc aaa gca aag gcg agg gcg atc	882
Asn Pro Glu Ser Ala Asp Leu Arg Ala Leu Ala Lys His Leu Tyr Asp	
235 240 245	
ttg aca gga aag aca aca gac aaa tca cca ttc gtt atc tat gac atg	930
Ser Tyr Ile Lys Ser Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile	
250 255 260	
aat tcc tta atg atg gga gaa gat aaa atc aag ttc aaa cac atc acc	978
Leu Thr Gly Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met	
265 270 275 280	
ccc ctg cag gag cag agc aaa gag gtg gcc atc cgc atc ttt cag ggc	1026
Asn Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr	
285 290 295	
tgc cag ttt cgc tcc gtg gag gct gtg cag gag atc aca gag tat gcc	1074
Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly	
300 305 310	
aaa agc att cct ggt ttt gta aat ctt gac ttg aac gac caa gta act	1122
Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala	
315 320 325	
ctc ctc aaa tat gga gtc cac gag atc att tac aca atg ctg gcc tcc	1170
Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr	
330 335 340	
ttg atg aat aaa gat ggg gtt ctc ata tcc gag ggc caa ggc ttc atg	1218
Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser	
345 350 355 360	
aca agg gag ttt cta aag agc ctg cga aag cct ttt ggt gac ttt atg	1266
Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met	
365 370 375	
gag ccc aag ttt gag ttt gct gtg aag ttc aat gca ctg gaa tta gat	1314
Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met	
380 385 390	
gac agc gac ttg gca ata ttt att gct gtc att att ctc agt gga gac	1362
Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp	
395 400 405	

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cgc cca ggt ttg ctg aat gtg aag ccc att gaa gac att caa gac aac 1410  
 Asp Ser Asp Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp  
 410 415 420

ctg cta caa gcc ctg gag ctc cag ctg aag ctg aac cac cct gag tcc 1458  
 Arg Pro Gly Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn  
 425 430 435 440

tca cag ctg ttt gcc aag ctg ctc cag aaa atg aca gac ctc aga cag 1506  
 Leu Leu Gln Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser  
 445 450 455

att gtc acg gaa cac gtg cag cta ctg cag gtg atc aag aag acg gag 1554  
 Ser Gln Leu Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln  
 460 465 470

aca gac atg agt ctt cac ccg ctc ctg cag gag atc tac aag gac ttg 1602  
 Ile Val Thr Glu His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu  
 475 480 485

tac tag 1608  
 Thr Asp Met Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu  
 490 495 500

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 <212> PRT  
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<400> 16  
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 20 25 30  
 Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val  
 35 40 45  
 Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro  
 50 55 60  
 Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp  
 65 70 75 80  
 Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp  
 85 90 95  
 Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser  
 100 105 110  
 Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu  
 115 120 125  
 Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp  
 130 135 140  
 Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys  
 145 150 155 160  
 Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys  
 165 170 175  
 Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr  
 180 185 190

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Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	His	Asn	Ala	Ile	
		195					200					205				
Arg	Phe	Gly	Arg	Met	Pro	Gln	Ala	Glu	Lys	Glu	Lys	Leu	Leu	Ala	Glu	
		210				215					220					
Ile	Ser	Ser	Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	Ala	Asp	Leu	Arg	
225					230					235					240	
Ala	Leu	Ala	Lys	His	Leu	Tyr	Asp	Ser	Tyr	Ile	Lys	Ser	Phe	Pro	Leu	
				245					250					255		
Thr	Lys	Ala	Lys	Ala	Arg	Ala	Ile	Leu	Thr	Gly	Lys	Thr	Thr	Asp	Lys	
			260					265						270		
Ser	Pro	Phe	Val	Ile	Tyr	Asp	Met	Asn	Ser	Leu	Met	Met	Gly	Glu	Asp	
		275					280					285				
Lys	Ile	Lys	Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	Glu	Gln	Ser	Lys	Glu	
		290				295					300					
Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	Arg	Ser	Val	Glu	Ala	
305					310					315					320	
Val	Gln	Glu	Ile	Thr	Glu	Tyr	Ala	Lys	Ser	Ile	Pro	Gly	Phe	Val	Asn	
					325				330					335		
Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	Leu	Lys	Tyr	Gly	Val	His	Glu		
			340					345					350			
Ile	Ile	Tyr	Thr	Met	Leu	Ala	Ser	Leu	Met	Asn	Lys	Asp	Gly	Val	Leu	
		355					360						365			
Ile	Ser	Glu	Gly	Gln	Gly	Phe	Met	Thr	Arg	Glu	Phe	Leu	Lys	Ser	Leu	
		370				375					380					
Arg	Lys	Pro	Phe	Gly	Asp	Phe	Met	Glu	Pro	Lys	Phe	Glu	Phe	Ala	Val	
385					390					395					400	
Lys	Phe	Asn	Ala	Leu	Glu	Leu	Asp	Asp	Ser	Asp	Leu	Ala	Ile	Phe	Ile	
				405					410					415		
Ala	Val	Ile	Ile	Leu	Ser	Gly	Asp	Arg	Pro	Gly	Leu	Leu	Asn	Val	Lys	
			420					425						430		
Pro	Ile	Glu	Asp	Ile	Gln	Asp	Asn	Leu	Leu	Gln	Ala	Leu	Glu	Leu	Gln	
		435					440						445			
Leu	Lys	Leu	Asn	His	Pro	Glu	Ser	Ser	Gln	Leu	Phe	Ala	Lys	Leu	Leu	
		450				455					460					
Gln	Lys	Met	Thr	Asp	Leu	Arg	Gln	Ile	Val	Thr	Glu	His	Val	Gln	Leu	
465					470					475					480	
Leu	Gln	Val	Ile	Lys	Lys	Thr	Glu	Thr	Asp	Met	Ser	Leu	His	Pro	Leu	
				485					490					495		
Leu	Gln	Glu	Ile	Tyr	Lys	Asp	Leu	Tyr								
			500					505								

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 <212> DNA  
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 gcattgactc acagagcagc a

21

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 <212> DNA  
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<400> 18  
 gctcaacagc accctgga

18

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<210> 19  
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 <212> DNA  
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<210> 20  
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<400> 21  
 cattacggag agatccacgg 20

<210> 22  
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<220>  
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 <222> (161)...(2596)

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 agccccgagc cctcggcggg ctgcgagcga ctccccggcg atg cct cac aac tcc 175  
 Met Pro His Asn  
 1

atc aga tct ggc cat gga ggg ctg aac cag ctg gga ggg gcc ttt gtg 223  
 Ser  
 5

aat ggc aga cct ctg ccg gaa gtg gtc cgc cag cgc atc gta gac ctg 271  
 Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu Gly Gly Ala Phe Val  
 10 15 20

gcc cac cag ggt gta agg ccc tgc gac atc tct cgc cag ctc cgc gtc 319  
 Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln Arg Ile Val Asp Leu  
 25 30 35

agc cat ggc tgc gtc agc aag atc ctt ggc agg tac tac gag act ggc 367  
 Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser Arg Gln Leu Arg Val  
 40 45 50

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agc atc cgg cct gga gtg ata ggg ggc tcc aag ccc aag gtg gcc acc	415
Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg Tyr Tyr Glu Thr Gly	
55 60 65	
ccc aag gtg gtg gag aag att ggg gac tac aaa cgc cag aac cct acc	463
Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys Pro Lys Val Ala Thr	
70 75 80 85	
atg ttt gcc tgg gag atc cga gac cgg ctc ctg gct gag ggc gtc tgt	511
Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys Arg Gln Asn Pro Thr	
90 95 100	
gac aat gac act gtg ccc agt gtc agc tcc att aat aga atc atc cgg	559
Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu Ala Glu Gly Val Cys	
105 110 115	
acc aaa gtg cag caa cca ttc aac ctc cct atg gac agc tgc gtg gcc	607
Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile Asn Arg Ile Ile Arg	
120 125 130	
acc aag tcc ctg agt ccc gga cac acg ctg atc ccc agc tca gct gta	655
Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met Asp Ser Cys Val Ala	
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Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile Pro Ser Ser Ala Val	
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Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu Gly Ser Thr Tyr Ser	
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Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly Ser Asp Lys Arg Lys	
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Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu Ser Ile Asp Ser Gln	
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Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg Thr Asp Ala Phe Ser	
215 220 225	
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Gln His His Leu Glu Pro Leu Glu Cys Pro Phe Glu Arg Gln His Tyr	
230 235 240 245	
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Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys Gly Glu Gln Gly Leu	
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ctg acc cct tcc aac acg cca ctg ggg cgc aac ctc tcg act cac cag	1039
Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp Asp Gly Lys Ala Thr	
265 270 275	

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Thr Tyr Pro Val Val Ala Gly Arg Glu Met Val Gly Pro Thr Leu Pro	
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tct gcc atc gca ggc atg gtg gca gaa atg acc atg gtt gac aca gag	1183
Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly Ser Tyr Ala Ser	
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Ser Ala Ile Ala Gly Met Val Ala Glu Met Thr Met Val Asp Thr Glu	
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Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val Asp Leu Ser	
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Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro Phe Thr Thr	
360 365 370	
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Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp Ile Pro Phe	
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Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp Leu Lys Leu	
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Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser Pro Pro Tyr	
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aac tcc ctc atg gca att gaa tgt cgt gtc tgt gga gat aaa gct tct	1519
Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu Glu Pro Ser	
425 430 435	
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Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp Lys Ala Ser	
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cgg aga aca atc aga ttg aag ctt atc tat gac aga tgt gat ctt aac	1615
Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe	
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Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys Asp Leu Asn	
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Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr Cys Arg Phe	
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gca ctg gaa tta gat gac agc gac ttg gca ata ttt att gct gtc att Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn 695 700 705	2335
att ctc agt gga gac cgc cca ggt ttg ctg aat gtg aag ccc att gaa Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala Val Ile 710 715 720 725	2383

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aac cac cct gag tcc tca cag ctg ttt gcc aag ctg ctc cag aaa atg	2479
Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln Leu Lys Leu	
745 750 755	
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Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu Gln Lys Met	
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atc aag aag acg gag aca gac atg agt ctt cac ccg ctc ctg cag gag	2575
Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu Leu Gln Val	
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Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys	
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Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys	
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Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu	
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Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile	
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Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu	
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Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly	
180 185 190	
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu	
195 200 205	
Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg	
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0976544-01304



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Glu	Arg	Gln	His	Tyr	Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys
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Gly	Glu	Gln	Gly	Leu	Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp
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Asp	Gly	Lys	Ala	Thr	Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	Gly	Arg	Asn
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Leu	Ser	Thr	His	Gln	Thr	Tyr	Pro	Val	Val	Ala	Gly	Arg	Glu	Met	Val
	290					295					300				
Gly	Pro	Thr	Leu	Pro	Gly	Tyr	Pro	Pro	His	Ile	Pro	Thr	Ser	Gly	Gln
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Gly	Ser	Tyr	Ala	Ser	Ser	Ala	Ile	Ala	Gly	Met	Val	Ala	Glu	Met	Thr
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Met	Val	Asp	Thr	Glu	Met	Pro	Phe	Trp	Pro	Thr	Asn	Phe	Gly	Ile	Ser
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Ser	Val	Asp	Leu	Ser	Val	Met	Glu	Asp	His	Ser	His	Ser	Phe	Asp	Ile
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Lys	Pro	Phe	Thr	Thr	Val	Asp	Phe	Ser	Ser	Ile	Ser	Thr	Pro	His	Tyr
	370					375					380				
Glu	Asp	Ile	Pro	Phe	Thr	Arg	Thr	Asp	Pro	Val	Val	Ala	Asp	Tyr	Lys
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Tyr	Asp	Leu	Lys	Leu	Gln	Glu	Tyr	Gln	Ser	Ala	Ile	Lys	Val	Glu	Pro
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Ala	Ser	Pro	Pro	Tyr	Tyr	Ser	Glu	Lys	Thr	Gln	Leu	Tyr	Asn	Lys	Pro
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His	Glu	Glu	Pro	Ser	Asn	Ser	Leu	Met	Ala	Ile	Glu	Cys	Arg	Val	Cys
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Gly	Asp	Lys	Ala	Ser	Gly	Phe	His	Tyr	Gly	Val	His	Ala	Cys	Glu	Gly
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Cys	Lys	Gly	Phe	Phe	Arg	Arg	Thr	Ile	Arg	Leu	Lys	Leu	Ile	Tyr	Asp
465					470					475					480
Arg	Cys	Asp	Leu	Asn	Cys	Arg	Ile	His	Lys	Lys	Ser	Arg	Asn	Lys	Cys
				485					490					495	
Gln	Tyr	Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	His	Asn
			500					505					510		
Ala	Ile	Arg	Phe	Gly	Arg	Met	Pro	Gln	Ala	Glu	Lys	Glu	Lys	Leu	Leu
		515					520					525			
Ala	Glu	Ile	Ser	Ser	Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	Ala	Asp
	530					535					540				
Leu	Arg	Ala	Leu	Ala	Lys	His	Leu	Tyr	Asp	Ser	Tyr	Ile	Lys	Ser	Phe
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Pro	Leu	Thr	Lys	Ala	Lys	Ala	Arg	Ala	Ile	Leu	Thr	Gly	Lys	Thr	Thr
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Asp	Lys	Ser	Pro	Phe	Val	Ile	Tyr	Asp	Met	Asn	Ser	Leu	Met	Met	Gly
			580					585					590		
Glu	Asp	Lys	Ile	Lys	Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	Glu	Gln	Ser
	595						600					605			
Lys	Glu	Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	Arg	Ser	Val
	610					615					620				
Glu	Ala	Val	Gln	Glu	Ile	Thr	Glu	Tyr	Ala	Lys	Ser	Ile	Pro	Gly	Phe
625					630					635					640
Val	Asn	Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	Tyr	Gly	Val
				645					650					655	
His	Glu	Ile	Ile	Tyr	Thr	Met	Leu	Ala	Ser	Leu	Met	Asn	Lys	Asp	Gly
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				Met Pro His Asn Ser											
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atc aga tct ggc cat gga ggg ctg aac cag ctg gga ggg gcc ttt gtg	223														
Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu Gly Gly Ala Phe Val															
	10 15 20														
aat ggc aga cct ctg ccg gaa gtg gtc cgc cag cgc atc gta gac ctg	271														
Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln Arg Ile Val Asp Leu															
	25 30 35														
gcc cac cag ggt gta agg ccc tgc gac atc tct cgc cag ctc cgc gtc	319														
Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser Arg Gln Leu Arg Val															
	40 45 50														
agc cat ggc tgc gtc agc aag atc ctt ggc agg tac tac gag act ggc	367														
Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg Tyr Tyr Glu Thr Gly															
	55 60 65														
agc atc cgg cct gga gtg ata ggg ggc tcc aag ccc aag gtg gcc acc	415														
Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys Pro Lys Val Ala Thr															
	70 75 80 85														
ccc aag gtg gtg gag aag att ggg gac tac aaa cgc cag aac cct acc	463														

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				90					95					100		
atg	ttt	gcc	tgg	gag	atc	cga	gac	cgg	ctc	ctg	gct	gag	ggc	gtc	tgt	511
Met	Phe	Ala	Trp	Glu	Ile	Arg	Asp	Arg	Leu	Leu	Ala	Glu	Gly	Val	Cys	
			105					110					115			
gac	aat	gac	act	gtg	ccc	agt	gtc	agc	tcc	att	aat	aga	atc	atc	cgg	559
Asp	Asn	Asp	Thr	Val	Pro	Ser	Val	Ser	Ser	Ile	Asn	Arg	Ile	Ile	Arg	
			120					125				130				
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Thr	Lys	Val	Gln	Gln	Pro	Phe	Asn	Leu	Pro	Met	Asp	Ser	Cys	Val	Ala	
			135				140					145				
acc	aag	tcc	ctg	agt	ccc	gga	cac	acg	ctg	atc	ccc	agc	tca	gct	gta	655
Thr	Lys	Ser	Leu	Ser	Pro	Gly	His	Thr	Leu	Ile	Pro	Ser	Ser	Ala	Val	
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Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	Asp	Ser	Leu	Gly	Ser	Thr	Tyr	Ser	
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atc	aat	ggg	ctc	ctg	ggc	atc	gct	cag	cct	ggc	agc	gac	aag	agg	aaa	751
Ile	Asn	Gly	Leu	Leu	Gly	Ile	Ala	Gln	Pro	Gly	Ser	Asp	Lys	Arg	Lys	
			185					190					195			
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Met	Asp	Asp	Ser	Asp	Gln	Asp	Ser	Cys	Arg	Leu	Ser	Ile	Asp	Ser	Gln	
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Ser	Ser	Ser	Ser	Gly	Pro	Arg	Lys	His	Leu	Arg	Thr	Asp	Ala	Phe	Ser	
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cag	cac	cac	ctc	gag	ccg	ctc	gag	tgc	cca	ttt	gag	cgg	cag	cac	tac	895
Gln	His	His	Leu	Glu	Pro	Leu	Glu	Cys	Pro	Phe	Glu	Arg	Gln	His	Tyr	
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Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys	Gly	Glu	Gln	Gly	Leu	
				250					255					260		
tac	ccg	ctg	ccc	ttg	ctc	aac	agc	acc	ctg	gac	gac	ggg	aag	gcc	acc	991
Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp	Asp	Gly	Lys	Ala	Thr	
			265					270					275			
ctg	acc	cct	tcc	aac	acg	cca	ctg	ggg	cgc	aac	ctc	tcg	act	cac	cag	1039
Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	Gly	Arg	Asn	Leu	Ser	Thr	His	Gln	
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Thr	Tyr</															

Glu Thr Pro Glu Val Ser Ser Ser Ser Ser Thr Pro Cys Ser Leu Ser	
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Gln Ala Leu Leu Ser Gly Arg Glu Met Val Gly Pro Thr Leu Pro Gly	
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Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly Ser Tyr Ala Ser Ser	
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Pro	Lys	Val	Ala	Thr	Pro	Lys	Val	Val	Glu	Lys	Ile	Gly	Asp	Tyr	Lys
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Arg	Gln	Asn	Pro	Thr	Met	Phe	Ala	Trp	Glu	Ile	Arg	Asp	Arg	Leu	Leu
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Ala	Glu	Gly	Val	Cys	Asp	Asn	Asp	Thr	Val	Pro	Ser	Val	Ser	Ser	Ile
		115					120					125			
Asn	Arg	Ile	Ile	Arg	Thr	Lys	Val	Gln	Gln	Pro	Phe	Asn	Leu	Pro	Met
		130				135					140				
Asp	Ser	Cys	Val	Ala	Thr	Lys	Ser	Leu	Ser	Pro	Gly	His	Thr	Leu	Ile
145					150					155				160	
Pro	Ser	Ser	Ala	Val	Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	Asp	Ser	Leu
			165					170					175		
Gly	Ser	Thr	Tyr	Ser	Ile	Asn	Gly	Leu	Leu	Gly	Ile	Ala	Gln	Pro	Gly
		180					185						190		
Ser	Asp	Lys	Arg	Lys	Met	Asp	Asp	Ser	Asp	Gln	Asp	Ser	Cys	Arg	Leu
	195					200						205			
Ser	Ile	Asp	Ser	Gln	Ser	Ser	Ser	Gly	Pro	Arg	Lys	His	Leu	Arg	
	210				215					220					
Thr	Asp	Ala	Phe	Ser	Gln	His	His	Leu	Glu	Pro	Leu	Glu	Cys	Pro	Phe
225					230					235				240	
Glu	Arg	Gln	His	Tyr	Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys
			245					250					255		
Gly	Glu	Gln	Gly	Leu	Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp
			260					265					270		
Asp	Gly	Lys	Ala	Thr	Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	Gly	Arg	Asn
		275					280					285			
Leu	Ser	Thr	His	Gln	Thr	Tyr	Pro	Val	Val	Ala	Asp	Pro	His	Ser	Pro
	290				295						300				
Leu	Ala	Ile	Lys	Gln	Glu	Thr	Pro	Glu	Val	Ser	Ser	Ser	Ser	Ser	Thr
305					310					315				320	
Pro	Cys	Ser	Leu	Ser	Ser	Ser	Ala	Leu	Leu	Asp	Leu	Gln	Gln	Val	Gly
			325					330					335		
Ser	Gly	Val	Pro	Pro	Phe	Asn	Ala	Phe	Pro	His	Ala	Ala	Ser	Val	Tyr
		340					345						350		
Gly	Gln	Phe	Thr	Gly	Gln	Ala	Leu	Leu	Ser	Gly	Arg	Glu	Met	Val	Gly
		355				360						365			
Pro	Thr	Leu	Pro	Gly	Tyr	Pro	Pro	His	Ile	Pro	Thr	Ser	Gly	Gln	Gly
	370				375						380				
Ser	Tyr	Ala	Ser	Ser	Ala	Ile	Ala	Gly	Met	Val	Ala	Gly	Ser	Glu	Tyr
385					390					395				400	

0976544.044004

Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu Ala  
 405 410 415  
 Trp Gly Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Ser  
 420 425 430  
 Ser Thr Ser Arg Pro Ser Ala Pro Pro Thr Thr Ala Thr Ala Phe Asp  
 435 440 445  
 His Leu  
 450

<210> 26  
 <211> 1811  
 <212> DNA  
 <213> Homo Sapiens  
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 <222> (173)...(1609)

<400> 26

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 ggctggcctc gaggacaccg gagaggggcg ccacgccgcc gtggccgcag aa atg acc 178  
 Met Thr  
 1

atg gtt gac aca gag atc gca ttc tgg ccc acc aac ttt ggg atc agc 226  
 Met Val Asp Thr Glu Ile Ala Phe Trp Pro Thr Asn Phe Gly Ile Ser  
 5 10 15

tcc gtg gat ctc tcc gta atg gaa gac cac tcc cac tcc ttt gat atc 274  
 Ser Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile  
 20 25 30

aag ccc ttc act act gtt gac ttc tcc agc att tct act cca cat tac 322  
 Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr  
 35 40 45 50

gaa gac att cca ttc aca aga aca gat cca gtg gtt gca gat tac aag 370  
 Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys  
 55 60 65

tat gac ctg aaa ctt caa gag tac caa agt gca atc aaa gtg gag cct 418  
 Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro  
 70 75 80

gca tct cca cct tat tat tct gag aag act cag ctc tac aat aag cct 466  
 Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro  
 85 90 95

cat gaa gag cct tcc aac tcc ctc atg gca att gaa tgt cgt gtc tgt 514  
 His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys  
 100 105 110

gga gat aaa gct tct gga ttt cac tat gga gtt cat gct tgt gaa gga 562  
 Gly Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly  
 115 120 125 130

0975444 044804

tgc aag ggt ttc ttc cgg aga aca atc aga ttg aag ctt atc tat gac Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp 135 140 145	610
aga tgt gat ctt aac tgt cgg atc cac aaa aaa agt aga aat aaa tgt Arg Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys 150 155 160	658
cag tac tgt cgg ttt cag aaa tgc ctt gca gtg ggg atg tct cat aat Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn 165 170 175	706
gcc atc agg ttt ggg cgg atc gca cag gcc gag aag gag aag ctg ttg Ala Ile Arg Phe Gly Arg Ile Ala Gln Ala Glu Lys Glu Lys Leu Leu 180 185 190	754
gcg gag atc tcc agt gat atc gac cag ctg aat cca gag tcc gct gac Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp 195 200 205 210	802
ctc cgt cag gcc ctg gca aaa cat ttg tat gac tca tac ata aag tcc Leu Arg Gln Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser 215 220 225	850
ttc ccg ctg acc aaa gca aag gcg agg gcg atc ttg aca gga aag aca Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr 230 235 240	898
aca gac aaa tca cca ttc gtt atc tat gac atg aat tcc tta atg atg Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met 245 250 255	946
gga gaa gat aaa atc aag ttc aaa cac atc acc ccc ctg cag gag cag Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln 260 265 270	994
agc aaa gag gtg gcc atc cgc atc ttt cag ggc tgc cag ttt cgc tcc Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser 275 280 285 290	1042
gtg gag gct gtg cag gag atc aca gag tat gcc aaa agc att cct ggt Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly 295 300 305	1090
ttt gta aat ctt gac ttg aac gac caa gta act ctc ctc aaa tat gga Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly 310 315 320	1138
gtc cac gag atc att tac aca atg ctg gcc tcc ttg atg aat aaa gat Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp 325 330 335	1186
ggg gtt ctc ata tcc gag ggc caa ggc ttc atg aca agg gag ttt cta Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu 340 345 350	1234

0076511.041304

aag agc ctg cga aag cct ttt ggt gac ttt atg gag ccc aag ttt gag 1282  
 Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu  
 355 360 365 370

ttt gct gtg aag ttc aat gca ctg gaa tta gat gac agc gac ttg gca 1330  
 Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala  
 375 380 385

ata ttt att gct gtc att att ctc agt gga gac cgc cca ggt ttg ctg 1378  
 Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu  
 390 395 400

aat gtg aag ccc att gaa gac att caa gac aac ctg cta caa gcc ctg 1426  
 Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu  
 405 410 415

gag ctc cag ctg aag ctg aac cac cct gag tcc tca cag ctg ttt gcc 1474  
 Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala  
 420 425 430

aag ctg ctc cag aaa atg aca gac ctc aga cag att gtc acg gaa cac 1522  
 Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His  
 435 440 445 450

gtg cag cta ctg cag gtg atc aag aag acg gag aca gac atg agt ctt 1570  
 Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu  
 455 460 465

cac ccg ctc ctg cag gag atc tac aag gac ttg tac tag cagagagtcc 1619  
 His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr \*  
 470 475

tgagccactg ccaacatttc ctttcttcca gttgcactat tctgagggaa aatctgacca 1679  
 taagaaattt actgtgaaaa agcgtttttaa aaagaaaagg gtttagaata tgatctattt 1739  
 tatgcatatt gtttataaag acacattttac aattttacttt taatattaaa aattaccata 1799  
 ttatgaaatt gc 1811

<210> 27  
 <211> 478  
 <212> PRT  
 <213> Homo Sapiens

<400> 27  
 Met Thr Met Val Asp Thr Glu Ile Ala Phe Trp Pro Thr Asn Phe Gly  
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 Ile Ser Ser Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe  
 20 25 30  
 Asp Ile Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro  
 35 40 45  
 His Tyr Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp  
 50 55 60  
 Tyr Lys Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val  
 65 70 75 80  
 Glu Pro Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn  
 85 90 95

0976544-011894



Lys Pro His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg  
 100 105 110  
 Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys  
 115 120 125  
 Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile  
 130 135 140  
 Tyr Asp Arg Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn  
 145 150 155 160  
 Lys Cys Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser  
 165 170 175  
 His Asn Ala Ile Arg Phe Gly Arg Ile Ala Gln Ala Glu Lys Glu Lys  
 180 185 190  
 Leu Leu Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser  
 195 200 205  
 Ala Asp Leu Arg Gln Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile  
 210 215 220  
 Lys Ser Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly  
 225 230 235 240  
 Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu  
 245 250 255  
 Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln  
 260 265 270  
 Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe  
 275 280 285  
 Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile  
 290 295 300  
 Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys  
 305 310 315 320  
 Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn  
 325 330 335  
 Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu  
 340 345 350  
 Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys  
 355 360 365  
 Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp  
 370 375 380  
 Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly  
 385 390 395 400  
 Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln  
 405 410 415  
 Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu  
 420 425 430  
 Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr  
 435 440 445  
 Glu His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met  
 450 455 460  
 Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr  
 465 470 475

<210> 28  
 <211> 20  
 <212> DNA  
 <213> Homo Sapiens

<400> 28  
 gccaccaagt ccctgagtcc

<210> 29	
<211> 19	
<212> DNA	
<213> Homo Sapiens	
<400> 29	
gacctacggg aggaagccc	19
<210> 30	
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<400> 30	
gcggacccaa gcagtgg	18
<210> 31	
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<212> DNA	
<213> Homo Sapiens	
<400> 31	
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<210> 32	
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<212> DNA	
<213> Homo Sapiens	
<400> 32	
accagaaag cgattccttc a	21
<210> 33	
<211> 20	
<212> DNA	
<213> Homo Sapiens	
<400> 33	
atgggtgaaa ctctgggaga	20
<210> 34	
<211> 20	
<212> DNA	
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ttgctgcaga tccaaaaagg	20
<210> 35	
<211> 20	
<212> DNA	
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<400> 35	
gaggaagggg tggagctaga	20

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<210> 36  
 <211> 537  
 <212> DNA  
 <213> Homo Saiens

<220>  
 <223> n = A or T or C or G or other

<400> 36  
 atg ggt gaa act ctg gga gat tct cct att gac cca gaa agc gat tcc 48  
 ttc act gat aca ctg tct gca aac ata tca caa gaa nat cct cac tca 96  
 ccc ttc gcc ata aag cag gaa acc ccc gag gtg tcc agt tct agc tcc 144  
 acc cct tcc tct tta tct agc tcc gcc ttt ttg gat ctg cag caa gtc 192  
 ggc tcc ggg gtc ccg ccc ttc aat gcc ttt ccc cat gct gcc tcc gtg 240  
 tac ggg cag ttc acg ggc cag gcc ctc ctc tca ggg cga gag atg gtg 288  
 ggg ccc acg ctg ccc gga tac cca ccc cac atc ccc acc agc gga cag 336  
 ggc agc tat gcc tcc tct gcc atc gca ggc atg gtg gca gga agt gaa 384  
 tac tct ggc aat gcc tat ggc cac acc ccc tac tcc tcc tac agc gag 432  
 gcc tgg cgc ttc ccc aac tcc agc ttg ctg agt tcc cca tat tat tac 480  
 agt tcc aca tca agg ccg agt gca ccg ccc acc act gcc acg gcc ttt 528  
 gac cat ctg 537

<210> 37  
 <211> 348  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <223> n = A or T or C or G or other

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 atgggtgaaa ctctgggaga ttctcctatt gaccagaaaa gcgattcctt cactgataca 60  
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 ccaccccaca tccccaccag cggacagggc agctatgcct cctctgccat cgcaggcatg 180  
 gtggcaggaa gtgaatactc tggcaatgcc tatggccaca cccctactc ctctacagc 240  
 gaggcctggc gcttccccaa ctccagcttg ctgagttccc catattatta cagttccaca 300  
 tcaaggccga gtgcaccgcc caccactgcc acggcctttg accatctg 348

<210> 38  
 <211> 246  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <223> n = A or T or C or G or other

<400> 38  
 atgggtgaaa ctctgggaga ttctcctatt gaccagaaaa gcgattcctt cactgataca 60  
 ctgtctgcaa acatatcaca agaangaagt gaatactctg gcaatgccta tggccacacc 120  
 ccctactcct cctacagcga ggctggcgcc tccccaaact ccagcttgct gagttcccca 180  
 tattattaca gttccacatc aaggccgagt gcaccgcccc ccactgccac ggcccttgac 240  
 catctg 246

<210> 39  
 <211> 178

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<212> PRT

<213> Homo Sapiens

<220>

<223> Xaa = any amino acid

<400> 39

Met	Gly	Glu	Thr	Leu	Gly	Asp	Ser	Pro	Ile	Asp	Pro	Glu	Ser	Asp	Ser
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Phe	Thr	Asp	Thr	Leu	Ser	Ala	Asn	Ile	Ser	Gln	Glu	Xaa	Pro	His	Ser
			20					25					30		
Pro	Phe	Ala	Ile	Lys	Gln	Glu	Thr	Pro	Glu	Val	Ser	Ser	Ser	Ser	Ser
		35					40					45			
Thr	Pro	Ser	Ser	Leu	Ser	Ser	Ser	Ala	Phe	Leu	Asp	Leu	Gln	Gln	Val
	50					55					60				
Gly	Ser	Gly	Val	Pro	Pro	Phe	Asn	Ala	Phe	Pro	His	Ala	Ala	Ser	Val
65					70					75				80	
Tyr	Gly	Gln	Phe	Thr	Gly	Gln	Ala	Leu	Leu	Ser	Gly	Arg	Glu	Met	Val
				85					90					95	
Gly	Pro	Thr	Leu	Pro	Gly	Tyr	Pro	Pro	His	Ile	Pro	Thr	Ser	Gly	Gln
			100					105					110		
Gly	Ser	Tyr	Ala	Ser	Ser	Ala	Ile	Ala	Gly	Met	Val	Ala	Gly	Ser	Glu
		115					120					125			
Tyr	Ser	Gly	Asn	Ala	Tyr	Gly	His	Thr	Pro	Tyr	Ser	Ser	Tyr	Ser	Glu
	130					135					140				
Ala	Trp	Arg	Phe	Pro	Asn	Ser	Ser	Leu	Leu	Ser	Ser	Pro	Tyr	Tyr	Tyr
145					150					155				160	
Ser	Ser	Thr	Ser	Arg	Pro	Ala	Pro	Pro	Thr	Thr	Ala	Thr	Ala	Phe	Asp
				165					170					175	
His	Leu														

<210> 40

<211> 116

<212> PRT

<213> Homo Sapiens

<220>

<223> Xaa = any amino acid

<400> 40

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Phe	Thr	Asp	Thr	Leu	Ser	Ala	Asn	Ile	Ser	Gln	Glu	Xaa	Arg	Glu	Met
			20					25					30		
Val	Gly	Pro	Thr	Leu	Pro	Gly	Tyr	Pro	Pro	His	Ile	Pro	Thr	Ser	Gly
		35					40					45			
Gln	Gly	Ser	Tyr	Ala	Ser	Ser	Ala	Ile	Ala	Gly	Met	Val	Ala	Gly	Ser
	50					55					60				
Glu	Tyr	Ser	Gly	Asn	Ala	Tyr	Gly	His	Thr	Pro	Tyr	Ser	Ser	Tyr	Ser
65					70					75				80	
Glu	Ala	Trp	Arg	Phe	Pro	Asn	Ser	Ser	Leu	Leu	Ser	Ser	Pro	Tyr	Tyr
				85					90					95	
Tyr	Ser	Ser	Thr	Ser	Arg	Pro	Ser	Ala	Pro	Pro	Thr	Thr	Ala	Thr	Ala
			100					105					110		
Phe	Asp	His	Leu												

007641.01301

115

<210> 41  
<211> 82  
<212> PRT  
<213> Homo Sapiens

<220>  
<223> Xaa = any amino acid

<400> 41  
Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser  
1 5 10 15  
Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Xaa Ser Glu Tyr  
20 25 30  
Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu Ala  
35 40 45  
Trp Arg Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Tyr Ser  
50 55 60  
Ser Thr Ser Arg Pro Ser Ala Pro Pro Thr Thr Ala Thr Ala Phe Asp  
65 70 75 80  
His Leu

<210> 42  
<211> 43  
<212> DNA  
<213> Homo Sapiens

<220>  
<223> n = A or T or C or G or other

<221> CDS  
<222> (1)...(43)

<400> 42  
tct gca aac ata tca caa gaa nat cct cac tca ccc ttc gcc a  
Ser Ala Asn Ile Ser Gln Glu Xaa Pro His Ser Pro Phe Ala  
1 5 10

43

<210> 43  
<211> 14  
<212> PRT  
<213> Homo Sapiens

<220>  
<223> Xaa = any amino acid

<400> 43  
Ser Ala Asn Ile Ser Gln Glu Xaa Pro His Ser Pro Phe Ala  
1 5 10

<210> 44  
<211> 43  
<212> DNA

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<213> Homo Sapiens

<220>

<223> n = A or T or C or G or other

<221> CDS

<222> (1)...(43)

<400> 44

tct gca aac ata tca caa gaa ngg cga gag atg gtg ggg ccc a  
Ser Ala Asn Ile Ser Gln Glu Xaa Arg Glu Met Val Gly Pro  
1 5 10

43

<210> 45

<211> 14

<212> PRT

<213> Homo Sapiens

<220>

<223> Xaa = any amino acid

<400> 45

Ser Ala Asn Ile Ser Gln Glu Xaa Arg Glu Met Val Gly Pro  
1 5 10

<210> 46

<211> 43

<212> DNA

<213> Homo Sapiens

<220>

<223> n = a or T or C or G or other

<221> CDS

<222> (1)...(43)

<400> 46

tct gca aac ata tca caa gaa nga agt gaa tac tct ggc aat g  
Ser Ala Asn Ile Ser Gln Glu Xaa Ser Glu Tyr Ser Gly Asn  
1 5 10

43

<210> 47

<211> 14

<212> PRT

<213> Homo Sapiens

<220>

<223> Xaa = any amino acid

<400> 47

Ser Ala Asn Ile Ser Gln Glu Xaa Ser Glu Tyr Ser Gly Asn  
1 5 10

09765444.014304